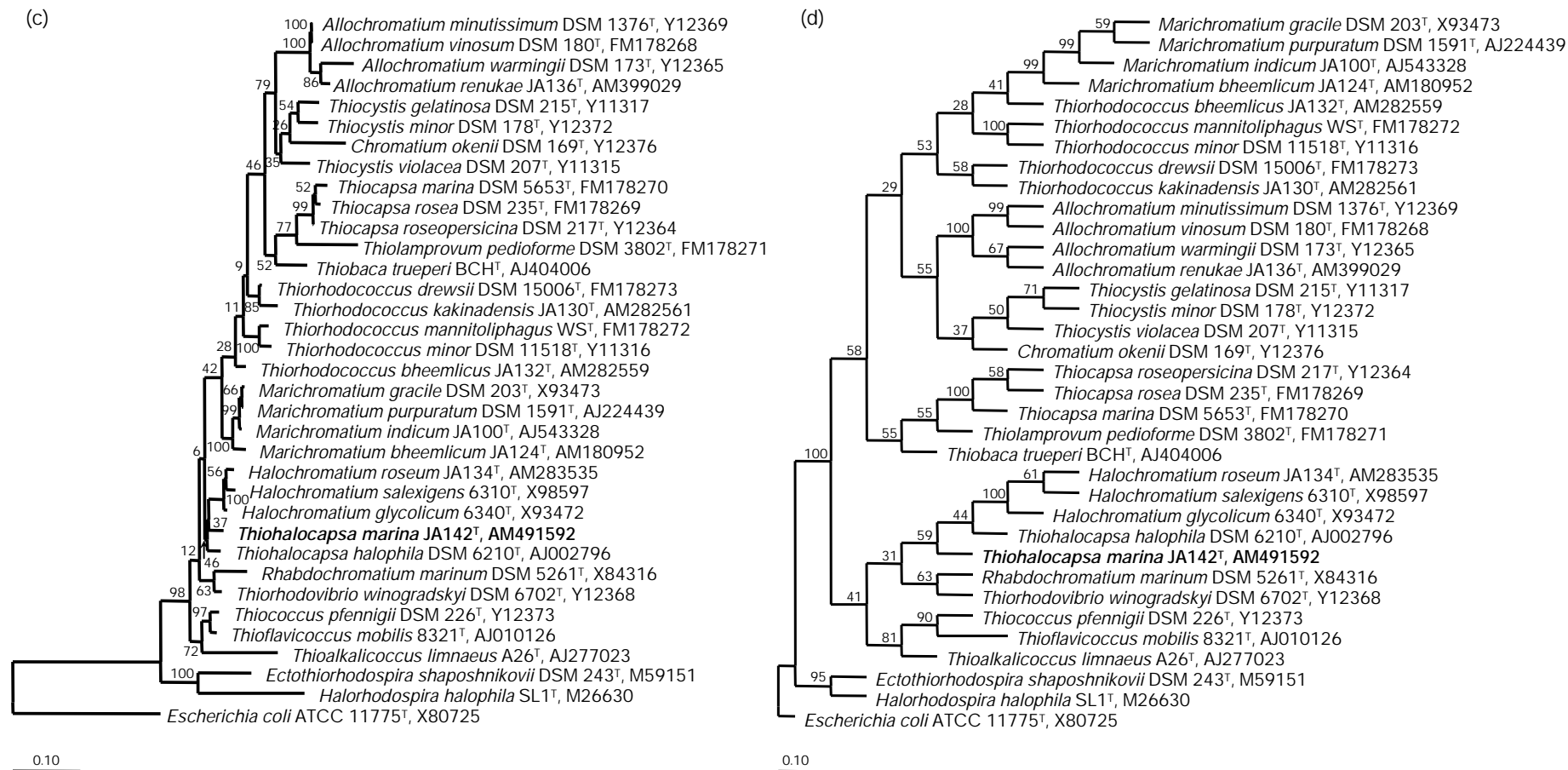


Supplementary Fig. S3. Phylogenetic trees based on 16S rRNA gene sequences showing the relationship of strain JA142^T within the family *Chromatiaceae* calculated by the neighbour-joining (a), maximum-likelihood (b), minimum-evolution (c) and maximum-parsimony (d) methods. Numbers at nodes represent bootstrap values from 100 replicates. Bars, 0.1 substitutions per alignment position.



Supplementary Fig. S3. cont.